

Functional Data

Monday 1pm

Scan (session=4, scan_idx=7)

Field:field=1

ScanUnit:unit_id=1, mask_id=1

ScanUnit:unit_id=2, mask_id=2

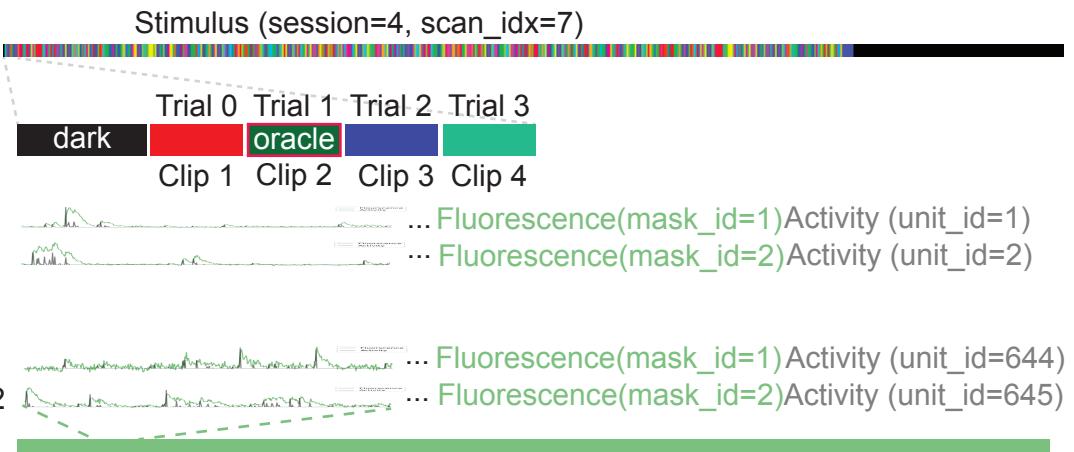
:

Field:field=2

ScanUnit:unit_id=644, mask_id=1

ScanUnit:unit_id=645, mask_id=2

:



Tuesday 3pm

Scan (session=5, scan_idx=6)

Field: field=1

ScanUnit:unit_id=1, mask_id=1

ScanUnit:unit_id=2, mask_id=2

:

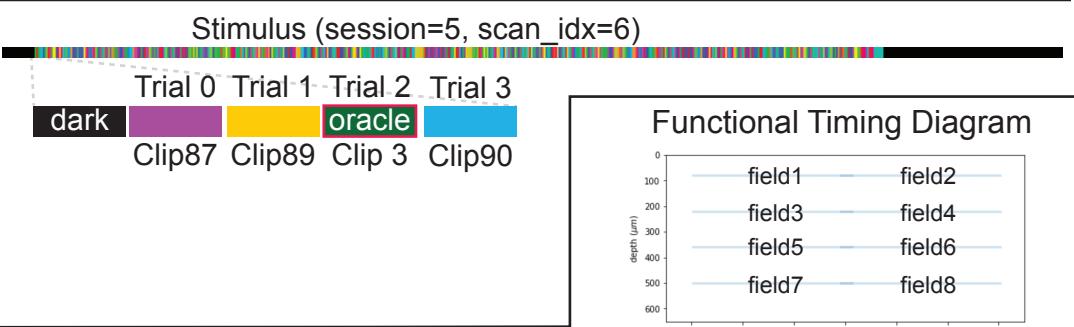
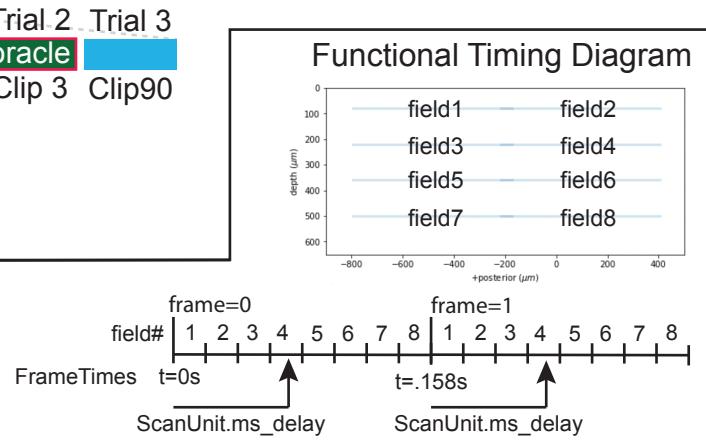
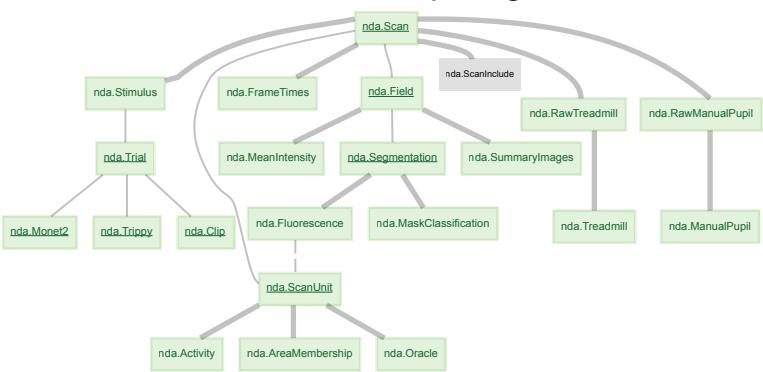


Table Relationship Diagram



Imaging data structure

nda.Scan: Scans are collections of frames that were acquired simultaneously. They are defined by a combination of session and scan index. Information on completed scans. Cajal Pipeline: [meso.ScanInfo](#)

nda.ScanInclude: Scans determined suitable for analysis. Some scans did not complete successfully or had incomplete data, and so are not recommended.

nda.Field: Individual fields of scans. Fields are single image planes. Each scans contains 8 fields. See [here](#) for a visualization of the scans to understand how the fields are distributed. Cajal Pipeline: [meso.ScanInfo.Field](#). On each frame of the scan, the microscope scanned one field, then hopped to the next field, and so on in a loop. So the individual 8 frames are spread out across the inter-scan frame time. All 8 frames were imaged within the 6.3Hz acquisition rate.

Timing and stimulus

nda.FrameTimes: Timestamps of scan frames in seconds relative to the start of the scan for the first pixel of the first imaging field. You can use this to get a precise timing of each unit in a consistent timebase.

nda.Stimulus: For each scan, contains the movie aligned to activity traces in **nda.Activity**. Note, this movie is now temporally downsampled to match the acquisition rate of the activity, but **does NOT reflect the temporal properties of the stimulus** that was actually shown to the animal. You have to download the actual stimulus movie at 30Hz if you want precise temporally correct information about the pixels shown to the mouse during the scan. (see below)

nda.Trial: Contains information for each trial of the movie in **nda.Stimulus**. There are three types of trials, **Clip**, **Monet2**, and **Trippy**. Each unique trial has its own **condition_hash**. To get detailed information for each trial stimulus, join each **condition_hash** according to its corresponding type in one of: **nda.Clip**, **nda.Monet2**, or **nda.Trippy**.

nda.Clip: Detailed information for movie clips.

nda.Monet2: Detailed information for the Monet2 stimulus.

nda.Trippy: Detailed information for the Trippy stimulus.

Functional analysis

nda.Oracle: Measures how reliably each ScanUnit responds to visual stimulus Leave-one-out correlation for repeated videos in stimulus.

nda.AreaMembership: Visual area labels for all units.

30Hz visual stimulus files

folder: https://bossdb-open-data.s3.amazonaws.com/iarpa_microns/minnie/functional_data/stimulus_movies

filename_format: f'stimulus_17797_{session}_{scan_idx}_v1.avi'

Dataset Preprint:

Functional connectomics spanning multiple areas of mouse visual cortex. nda docs:

bioRxiv 2021.07.28.454025; doi: <https://doi.org/10.1101/2021.07.28.454025> https://github.com/cajal/microns_phase3_nd